

Summative Assessment - Coefficient of Determination

We will once again use the `GSE17260_eset` data set with genomic information for 110 advanced-stage serious ovarian cancer patients. (A description can be found here <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0009615>)

Let's first load the data:

```
source("https://bioconductor.org/biocLite.R")
biocLite("curatedOvarianData")
library("curatedOvarianData")
source(system.file("extdata", "patientselection.config", package = "curatedOvarianData"))
data("GSE17260_eset")
set.seed(123)
```

Predict the expression of the gene in the first column using the expressions in columns 2, 3, ..., 11. The data can be obtained using the command

```
mat.gene = exprs(GSE17260_eset)
```

1. Select the variables of interest.
2. Fit an exploratory linear regression model for the variable of interest y .
3. Compute and report the R^2 value.